

CLAIMS

What is claimed is:

1. A carotenoid overproducing microorganism comprising the genes encoding a functional isoprenoid enzymatic biosynthetic pathway comprising a disrupted gene selected from the group consisting of *deaD*, *mreC*, and *yfhE*.
2. The carotenoid overproducing microorganism of Claim 1 wherein the isoprenoid enzymatic biosynthetic pathway comprises:
 - a) an upper isoprenoid enzymatic biosynthetic pathway comprising the genes *dxs*, *dxr*, *ygbP*, *ychB*, *ygbB*, *lytB*, *idi*, *ispA*, and *ispB*; and
 - b) a lower isoprenoid enzymatic biosynthetic pathway comprising the genes *crtE*, *crtB*, *crtI*, and *crtY*.
3. The carotenoid overproducing microorganism of Claim 2 wherein the lower pathway optionally comprises genes selected from the group consisting of *crtZ* and *crtW*.
4. The carotenoid overproducing microorganism of any of Claims 1 –3 or wherein the microorganism is selected from the group consisting of bacteria, yeasts and filamentous fungi.
5. The carotenoid overproducing microorganism of Claim 4 wherein the microorganism is selected from the group consisting *Aspergillus*, *Trichoderma*, *Saccharomyces*, *Pichia*, *Candida*, *Hansenula*, *Salmonella*, *Bacillus*, *Acinetobacter*, *Zymomonas*, *Agrobacterium*, *Erythrobacter*, *Chlorobium*, *Chromatium*, *Flavobacterium*, *Cytophaga*, *Rhodobacter*, *Rhodococcus*, *Streptomyces*, *Brevibacterium*, *Corynebacteria*, *Mycobacterium*, *Deinococcus*, *Paracoccus*, *Escherichia*, *Erwinia*, *Pantoea*, *Pseudomonas*, *Sphingomonas*, *Methylomonas*, *Methylobacter*, *Methylococcus*, *Methylosinus*, *Methylomicrobium*, *Methylocystis*, *Alcaligenes*, *Synechocystis*, *Synechococcus*, *Anabaena*, *Thiobacillus*, *Staphylococcus*, *Methanobacterium*, *Klebsiella*, and *Myxococcus*.

6. The carotenoid overproducing microorganism of Claim 5 wherein the microorganism is *E. coli*.
7. The carotenoid overproducing microorganism of either of Claims 2 or 3 wherein the lower pathway genes reside on an autonomously replicating plasmid.
8. The carotenoid overproducing microorganism of Claim 7 wherein the autonomously replicating plasmid comprises a replicon selected from the group consisting of p15A and pMB1.
9. The carotenoid overproducing microorganism of either of Claims 2 or 3 wherein the lower pathway genes are chromosomally integrated.
10. A carotenoid overproducing microorganism according to Claim 1 wherein the microorganism is *E. coli* and wherein the disrupted *deaD* gene has the sequence as set forth in SEQ ID NO: 36, the disrupted *mreC* gene has the sequence as set forth in SEQ ID NO: 40 and the disrupted *yfhE* has the sequence as set forth in SEQ ID NO: 42.
11. The carotenoid overproducing microorganism according to claim 10 optionally comprising mutations selected from the group consisting of: a mutation in the *thrS* gene as set forth in SEQ ID NO: 35, a mutation in the *rpsA* gene as set forth in SEQ ID NO: 37, a mutation in the *rpoC* gene as set forth in SEQ ID NO: 38, a mutation in the *yjeR* gene as set forth in SEQ ID NO: 39, and a mutation in the *rhoL* gene as set forth in SEQ ID NO: 41.
12. A carotenoid overproducing *E. coli* comprising:
 - a) an upper isoprenoid enzymatic biosynthetic pathway comprising the genes *dxs*, *dxr*, *ygbP*, *ychB*, *ygbB*, *lytB*, *idi*, *ispA*, and *ispB*;
 - b) a lower isoprenoid enzymatic biosynthetic pathway comprising the genes *crtE*, *crtB*, *crtI*, and *crtY*;
 - c) mutations selected from the group consisting of: a mutation in the *thrS* gene as set forth in SEQ ID NO: 35, a mutation in the *rpsA* gene as set forth in SEQ ID NO: 37, a mutation in the *rpoC* gene as set forth in SEQ ID NO: 38, a mutation in the *yjeR* gene as set forth in SEQ ID NO: 39, and a mutation in the *rhoL* gene as set forth in SEQ ID NO: 41;

wherein the genes of the lower isoprenoid enzymatic biosynthetic pathway reside on an autonomously replicating plasmid comprising a replicon selected from the group consisting of p15A and pMB1.

13. The carotenoid overproducing *E. coli* of Claim 12 wherein the lower pathway optionally comprises genes selected from the group consisting of *crtZ* and *crtW*.

14. A method for the production of a carotenoid comprising:
- a) contacting the carotenoid overproducing microorganism of any of Claims 1-3 with a fermentable carbon substrate;
 - b) growing the carotenoid overproducing microorganism of step (a) for a time sufficient to produce a carotenoid; and
 - c) optionally recovering the carotenoid from the carotenoid overproducing microorganism of step (b).

15. A method for the production of a carotenoid comprising:
- a) contacting the carotenoid overproducing *E. coli* of Claim 12 with a fermentable carbon substrate;
 - b) growing the carotenoid overproducing *E. coli* of step (a) for a time sufficient to produce a carotenoid; and
 - c) optionally recovering the carotenoid from the carotenoid overproducing microorganism of step (b).

16. A method according to either Claim 14 or 15 wherein the carotenoid is selected from the group consisting of antheraxanthin, adonixanthin, astaxanthin, canthaxanthin, capsorubrin, β -cryptoxanthin, didehydrolycopene, didehydrolycopene, β -carotene, ζ -carotene, δ -carotene, γ -carotene, keto- γ -carotene, ψ -carotene, ϵ -carotene, β, ψ -carotene, torulene, echinenone, gamma-carotene, zeta-carotene, alpha-cryptoxanthin, diatoxanthin, 7,8-didehydroastaxanthin, fucoxanthin, fucoxanthinol, isorenieratene, β -isorenieratene, lactucaxanthin, lutein, lycopene, neoxanthin, neurosporene, hydroxyneurosporene, peridinin, phytoene, rhodopin, rhodopin glucoside, siphonaxanthin, spheroidene, spheroidenone, spirilloxanthin, uriolide, uriolide acetate, violaxanthin, zeaxanthin- β -diglucoside, zeaxanthin, and C30-carotenoids.